

EXPLORING GLACIAL AND PRESENT EVOLUTIONARY PATTERNS OF A MARINE GOBY, *POMATOSCHISTUS MINUTUS*

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A classical understanding of marine fishes is that they have high effective population sizes and high levels of dispersal due to an apparent lack of barriers in the marine environment. The realization of a genetic population structure is therefore thought to be a slow process. To gain insights in this process, it is a challenge to disentangle the interaction between selection, gene flow, population history and genetic drift.

The sand goby (*Pomatoschistus minutus*), which is an important ecological but non-commercial species, was chosen to distinguish between natural and anthropologically induced processes. A spatio-temporal analysis with samples from different localities throughout the species distribution and with two types of genetic markers was performed to assess the neutral genetic population structure. Phylogeographical patterns were studied by sequence cytochrome *b* (mtDNA). Nine new nuclear microsatellites were developed and used to describe the current genetic diversity and population structure.

The genetic structure of the sand goby is best explained by a combination of present and historic factors. Due to its high potential for dispersion and high effective population size, it shows the typical features of a marine fish with a high level of diversity and a limited degree of genetic differentiation. The large genetic distance between the Venetian and all other samples shows that the sand gobies from the Adriatic Sea should be considered as a distinct cryptic species of the genus *Pomatoschistus*. Low but significant differentiation is observed between Atlantic and western Mediterranean *P. minutus*. In the Atlantic and Baltic basins, there is evidence for a postglacial range expansion and a weak pattern of isolation-by-distance. Furthermore the results support the hypothesis of a glacial refugium and a fine-scale genetic structure in the southern North Sea.

The neutral genetic pattern will be compared with putatively adaptive loci in order to study the genomic characteristics of local adaptation in the marine environment. This should provide a better understanding of how fish respond to changes in the environment.